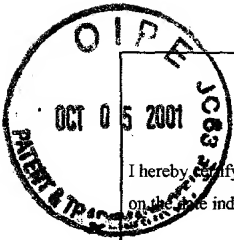


#6

PATENT
Docket No. 293102003000



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Tamara Alcaraz
Tamara Alcaraz

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Suresh K. TIKOO et al.

Serial No.: 09/871,212

Filing Date: May 31, 2001

For: MODIFIED BOVINE ADENOVIRUS
HAVING ALTERED TROPISM

Examiner: To Be Assigned

Group Art Unit: 1635

PRELIMINARY AMENDMENT

Box Missing Parts
Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

Prior to examination on the merits, Applicants respectfully request entry of this Preliminary Amendment for the above-identified patent application.

AMENDMENTS

In the specification:

On page 10, please amend the paragraph containing line 11, as follows:

Figures 1A-1S shows the complete nucleotide sequence of the BAV3 genome (SEQ ID NO: 1). In the polynucleotide sequence for BAV3, the penton regions starts at 12919 and ends at 14367; the hexon region starts at 17809 and ends at 20517; the fiber region starts at 27968 and ends at 30898. The knob domain of the fiber region starts after the 4 residues, TLWT, as shown in Figure 4 (SEQ ID NO: 2).

On page 10, please amend the paragraph containing line 20, as follows:

Figure 4 illustrates the characterization of BAV600 (SEQ ID NO: 2-4).

On page 11, please amend the paragraph containing line 9, as follow:

Figure 12 depicts the amino acid sequence for Human adenovirus 5 (HAV-5) fiber protein (SEQ ID NO: 5).

On page 11, please amend the paragraph containing line 11, as follows:

Figure 13 depicts the amino acid sequence for the Bovine Adenovirus-3 (BAV-3) fiber protein (SEQ ID NO: 6).

On page 11, please amend the paragraph containing line 13, as follows:

Figure 14 depicts the amino acid sequence of Ovine Adenovirus 287 fiber protein (SEQ ID NO: 7).

On page 11, please amend the paragraph containing line 15, as follows:

Figure 15 shows the amino acid sequence of Porcine Adenovirus-3 (PAV-3) fiber protein (SEQ ID NO: 8).

On page 11, please amend the paragraph containing line 17, as follows:

Figure 16 shows the amino acid sequence of Canine Adenovirus -2 (CAV-2) fiber protein (SEQ ID NO: 9).

On page 11, please amend the paragraph containing line 18, as follows:

Figures 17A-17G (SEQ ID NO: 5-9) depicts an amino acid alignment of various mammalian adenovirus fiber regions using the clustal method of the Multialign program.

On page 24, please amend the paragraph containing line 18, as follows:

Reddy *et al.* (1998) *Journal of Virology* 72:1394) disclose nucleotide sequences for BAV3. In the polynucleotide sequence for BAV3, the penton regions starts at 12919 and ends at 14367; the hexon region starts at 17809 and ends at 20517; the fiber region starts at 27968 and ends at 30898. The knob region (or domain) of the fiber protein starts after the residues TLWT motif as shown in Figure 4 (SEQ ID NO: 2-4). The fiber protein also contains shaft and tail regions (or domains).

On page 25, please amend the paragraph containing line 4, as follows:

Shayakhmetov *et al.*, *supra*, provide PCR primers for human Ad9 and human Ad35 fiber regions. The HAV-5 fiber protein is depicted in Figure 12 (SEQ ID NO: 5); Figure 13 (SEQ ID NO: 6) depicts the amino acid sequence for the Bovine Adenovirus-3 (BAV-3) fiber protein; Figure 14 (SEQ ID NO: 7) depicts the amino acid sequence of Ovine Adenovirus 287 fiber protein; Figure 15 (SEQ ID NO: 8) depicts the amino acid sequence of Porcine Adenovirus-3 (PAV-3) fiber protein; Figure 16 (SEQ ID NO: 9) depicts the amino acid sequence of Canine

Adenovirus -2 (CAV-2) fiber protein; and Figures 17A-17G (SEQ ID NO: 5-9) depicts an amino acid alignment of mammalian adenovirus fiber regions using the clustal method of the multialign program. The knob domain of the fiber regions typically starts after the amino acid residue motif TLWT (hinge region), see Figure 4 (SEQ ID NO: 2-4) (one exception is the ovine adenovirus fiber region).

Sequence Listing

Please insert the paper copy of the Sequence Listing after the abstract.

Adenovirus -2 (CAV-2) fiber protein; and Figures 17A-17G (SEQ ID NO: 5-9) depicts an amino acid alignment of mammalian adenovirus fiber regions using the clustal method of the multialign program. The knob domain of the fiber regions typically starts after the amino acid residue motif TLWT (hinge region), see Figure 4 (SEQ ID NO: 2-4) (one exception is the ovine adenovirus fiber region).

REMARKS

In compliance with 37 C.F.R. § 1.821 through § 1.825, applicants have amended the specification to add Sequence Identifiers. No new matter has been added by this amendment. Applicants respectfully request entry of the present amendment.

Attached hereto is a marked up version of the changes made to the specification by the current amendment with additions underlined and deletions bracketed. The attached pages are captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE".

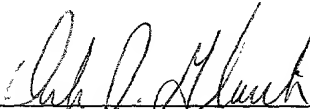
CONCLUSION

In the unlikely event that the Fee Transmittal is separated from this document and/or the Patent Office determines that an extension and/or other relief is required, applicants petition for any required relief including extensions of time and authorize the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to Deposit Account No. 03-1952 referencing docket no. 293102003000. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: October 5, 2001

By:



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Registration No. 33,888

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

MODIFIED BOVINE ADENOVIRUS HAVING ALTERED TROPISM

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